



SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> Mahajan, Pramod
Zuo, Zhuang

<120> Poly ADP-Ribose Polymerase Gene and its
Uses

<130> 5718-34

<140> US 09/236,995
<141> 1999-01-26

<150> US 60/072,785
<151> 1998-01-27

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<170> FastSEQ for Windows Version 4.0

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<213> Zea mays

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Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
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cgt ctt ggc aag atg gtt cag gcg tca cag ttc gac ggc ttc atg ccg 144
Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
35 40 45

atg tgg aac cat gcc agg tgc atc ttc agc aag aag aac cag ata aaa 192
Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
50 55 60

tcc gtt gac gat gtt gaa ggg ata gat gca ctt aga tgg gat gat caa 240
Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
65 70 75 80

gag aag ata cga aac tac gtt ggg agt gcc tca gct ggt aca agt tct 288

Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
 85 90 95

 aca gct gct cct cct gag aaa tgt aca att gag att gct cca tct gcc 336
 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
 100 105 110

 cgt act tca tgt aga cga tgc agt gaa aag att aca aaa gga tcg gtc 384
 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
 115 120 125

 cgt ctt tca gct aag ctt gag agt gaa ggt ccc aag ggt ata cca tgg 432
 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
 130 135 140

 tat cat gcc aac tgt ttc ttt gag gta tcc ccg tct gca act gtt gag 480
 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
 145 150 155 160

 aag ttc tca ggc tgg gat act ttg tcc gat gag gat aag aga acc atg 528
 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
 165 170 175

 ctc gat ctt gtt aaa aaa gat gtt ggc aac aat gaa caa aat aag ggt 576
 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
 180 185 190

 tcc aag cgc aag aaa agt gaa aat gat att gat agc tac aaa tcc gcc 624
 Ser Lys Arg Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
 195 200 205

 agg tta gat gaa agt aca tct gaa ggt aca gtg cga aac aaa ggg caa 672
 Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
 210 215 220

 ctt gta gac cca cgt ggt tcc aat act agt tca gct gat atc caa cta 720
 Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
 225 230 235 240

 aag ctt aag gag caa agt gac aca ctt tgg aag tta aag gat gga ctt 768
 Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
 245 250 255

 aag act cat gta tcg gct gct gaa tta agg gat atg ctt gag gct aat 816
 Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn
 260 265 270

 ggg cag gat aca tca gga cca gaa agg cac cta ttg gat cgc tgt gcg 864
 Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala
 275 280 285

 gat gga atg cta ttt gga gcg ctg ggt cct tgc cca gtc tgt gct aat 912
 Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
 290 295 300

 ggc atg tac tat tat aat ggt cag tac caa tgc agt ggt aat gtg tca 960

Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
 305 310 315 320

gag tgg tcc aag tgt aca tac tct gcc aca gaa cct gtc cgc gtt aag 1008
 Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
 325 330 335

aag aag tgg caa att cca cat gga aca aag aat gat tac ctt atg aag 1056
 Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
 340 345 350

tgg ttc aaa tct caa aag gtt aag aaa cca gag agg gtt ctt cca cca 1104
 Trp Phe Lys Ser Gln Lys Val Lys Pro Glu Arg Val Leu Pro Pro
 355 360 365

atg tca cct gag aaa tct gga agt aaa gca act cag aga aca tca ttg 1152
 Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
 370 375 380

ctg tct tct aaa ggg ttg gat aaa tta agg ttt tct gtt gta gga caa 1200
 Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
 385 390 395 400

tca aaa gaa gca gca aat gag tgg att gag aag ctc aaa ctt gct ggt 1248
 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
 405 410 415

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 gcc aac ttc tat gcc agg gtt gtc aaa gat att gat tgt tta att gca 1296
 Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
 420 425 430

tgt ggt gag ctc gac aat gaa aat gct gaa gtc agg aaa gca agg agg 1344
 Cys Gly Glu Leu Asp Asn Ala Glu Val Arg Lys Ala Arg Arg
 435 440 445

ctg aag ata cca att gta agg gag ggt tac att gga gaa tgt gtt aaa 1392
 Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
 450 455 460

aga aca aaa tgc tgc cat ttg att tgt ata aac tgg aat gcc tta gag 1440
 Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu
 465 470 475 480

tcc tca aaa ggc mgt act gtc act gtt aaa gtt aag ggc cga agt gct 1488
 Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala
 485 490 495

tgt tca tya agt cct cyg gtt tgc aag aat act gct cac att cct tra 1536
 Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa
 500 505 510

gra tgg gaa aag cat ata caa tgc amc ctt aaa cat gtt ctg acc tgn 1584
 Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa
 515 520 525

cac nag gtg tgy aca ggc tac tat gta ctc cag atc att gaa cag gat 1632

His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp
 530 535 540

gat ggg tct gag tgc tac gta ttt cgt aag tgg gga cgg gtt ggg agt 1680
 Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser
 545 550 555 560

gag aaa att gga ggg caa aaa ctg gag gag atg tca aaa act gag gca 1728
 Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala
 565 570 575

atc aag gaa ttc aaa aga tta ttt ctt gag aag act gga aac tca tgg 1776
 Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp
 580 585 590

gaa gct tgg gaa tgt aaa acc aat ttt cgg aag cag cct ggg aga ttt 1824
 Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe
 595 600 605

tac cca ctt gat gtt tat ggt gtt aag aaa gca cca aaa cgg aaa 1872
 Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
 610 615 620

gat atc agt gaa atg aaa agt tct ctt gct cct caa ttg cta gaa ctc 1920
 Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu
 625 630 635 640

atg aag atg ctt ttc aat gtg gag aca tat aga gct gct atg atg gaa 1968
 Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu
 645 650 655

ttt gaa awt aat atg tca gaa atg cct ctt ggg aag cta agc mag gra 2016
 Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa
 660 665 670

aat att gag raa gga ttt gaa gca tta act krg rta cmg rat tta ttt 2064
 Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe
 675 680 685

gaa gga cac cgc tna tca agc act ggc ttg ttr gag aaa gct naa ttg 2112
 Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu
 690 695 700

ttg ytg sga gcm ats syt ttt tca ctc tta tcc ctt cta ttc atc ctc 2160
 Leu Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu
 705 710 715 720

ata tta tac ggg atg agg atg att tca tat tca aag gcg aaa atg ctt 2208
 Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu
 725 730 735

gaa gct ctg cag gat att gaa att gct tca aag ata gtt ggc ttc gat 2256
 Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp
 740 745 750

agc gac agt gat gaa tct ctt gat gat aaa tat atg aaa ctt cac tgt 2304

Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys
 755 760 765

gac atc acc ccg ctg gct cac gat agt gaa gat tac aag tta att gag 2352
 Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu
 770 775 780

cag tat ctc ctc aac aca cat gct cct act cac aag gac tgg tcg ctg 2400
 Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu
 785 790 795 800

gaa ctg gag gaa gtt ttt tca ctt gat cga gat gga gaa ctt aat aag 2448
 Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys
 805 810 815

tac tca aga tat aaa aat aat ctg cat aac aag atg cta tta tgg cac 2496
 Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His
 820 825 830

ggt tca agg ttg acg aat ttt gtg gga att ctt agt caa ggg cta aga 2544
 Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg
 835 840 845

att gca cct cct gag gca cct gtt act ggc tat atg ttc ggc aaa ggc 2592
 Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly
 850 855 860

ctc tac ttt gca gat cta gta agc aag agc gca caa tac tgt tat gtg 2640
 Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val
 865 870 875 880

gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag gtt gct tta 2688
 Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu
 885 890 895

gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac aaa cct cca 2736
 Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro
 900 905 910

aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg gag 2784
 Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu
 915 920 925

tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc tgc ggc aag 2832
 Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys
 930 935 940

ccg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag tac 2880
 Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr.
 945 950 955 960

atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg ctg aag gtg 2928
 Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val
 965 970 975

cgt ttc cat cac aag agg tag 2949

Arg Phe His His Lys Arg *
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<213> Zea mays

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683, 684, 685, 686, 693, 699, 703, 706, 707, 708, 709, 710
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Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
35 40 45
Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
50 55 60
Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
65 70 75 80
Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
85 90 95
Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
100 105 110
Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
115 120 125
Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
130 135 140
Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
145 150 155 160
Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
165 170 175
Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
180 185 190
Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
195 200 205
Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
210 215 220
Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
225 230 235 240
Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
245 250 255
Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn,
260 265 270
Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala
275 280 285
Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
290 295 300
Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
305 310 315 320

B /
Cyst

Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
325 330 335
Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
340 345 350
Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
355 360 365
Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
370 375 380
Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
385 390 395 400
Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
405 410 415
Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
420 425 430
Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
435 440 445
Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
450 455 460
Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu
465 470 475 480
Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala
485 490 495
Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa
500 505 510
Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa
515 520 525
His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp
530 535 540
Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser
545 550 555 560
Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala
565 570 575
Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp
580 585 590
Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe
595 600 605
Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
610 615 620
Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu
625 630 635 640
Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu
645 650 655
Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa
660 665 670
Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Leu Phe
675 680 685
Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu
690 695 700
Leu Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu
705 710 715 720
Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu
725 730 735
Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp
740 745 750
Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys
755 760 765

Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu
 770 . 775 780
 Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu
 785 790 795 800
 Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys
 805 810 815
 Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His
 820 825 830
 Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg
 835 840 845
 Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly
 850 855 860
 Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val
 865 870 875 880
 Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu
 885 890 895
 Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro
 900 905 910
 Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu
 915 920 925
 Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys
 930 935 940
 Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr
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 Arg Phe His His Lys Arg
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 <213> Zea mays

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att ctt agt caa ggg cta aga att gca cct cct gag gca cct gtt act	96
Ile Leu Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr	
20 25 30	

ggc tat atg ttc ggc aaa ggc ctc tac ttt gca gat cta gta agc aag	144
Gly Tyr Met Phe Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys	
35 40 45	

agc gca caa tac tgt tat gtg gat agg aat aat cct gta ggt ttg atg	192
Ser Ala Gln Tyr Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met	
50 55 60	

ctt ctt tct gag gtt gct tta gga gac atg tat gaa cta aag aaa gcc	240
Leu Leu Ser Glu Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala	
65 70 75 80	
acg tcc atg gac aaa cct cca aga ggg aag cat tcg acc aag gga tta	288
Thr Ser Met Asp Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu	
85 90 95	
ggc aaa acc gtg cca ctg gag tca gag ttt gtg aag tgg agg gat gat	336
Gly Lys Thr Val Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp	
100 105 110	
gtc gta gtt ccc tgc ggc aag ccg gtg cca tca tca att agg agc tct	384
Val Val Val Pro Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser	
115 120 125	
gaa ctc atg tac aat gag tac atc gtc tac aac aca tcc cag gtg aag	432
Glu Leu Met Tyr Asn Glu Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys	
130 135 140	
atg cag ttc ttg ctg aag gtg cgt ttc cat cac aag agg tag	474
Met Gln Phe Leu Leu Lys Val Arg Phe His His Lys Arg *	
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*B
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<213> Zea mays

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Gly Tyr Met Phe Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys	
35 40 45	
Ser Ala Gln Tyr Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met	
50 55 60	
Leu Leu Ser Glu Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala	
65 70 75 80	
Thr Ser Met Asp Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu	
85 90 95	
Gly Lys Thr Val Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp	
100 105 110	
Val Val Val Pro Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser	
115 120 125	
Glu Leu Met Tyr Asn Glu Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys	
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Met Gln Phe Leu Leu Lys Val Arg Phe His His Lys Arg	
145 150 155	

<210> 5
<211> 530

<212> DNA
<213> Zea mays

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caagaagaac cagataaaat ccgttgcacga tggtaaggAG atagatgcac tttagatggGA 180
tgatcaagAG aagatacggAA actacgttgg gagtgccctca gctggtacAA gttctacAGC 240
tgctccctCTT gagaaatgtA caattgagAT tgctccatCT gcccgtactT catgttagACG 300
atgcagtGAA aagattacaA aaggatcgGT ccgttccTCA gctaagCTT agagtGAAGG 360
tccccaaGGT ataccatGGT atcatGCCAA ctgtttcttt gaggtatCCC cgtctgcaac 420
tggtaaggAG ttctcaggCT gggataACTT gtccgatgAG gataagAGAA ccatgctcgA 480
tcttgttAAA aaagatgttG gcaacaatGA acaaaATAAG ggttccaAGC 530

B1
Anello